Amendments to the Claims:

1. (currently amended) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

   a) has a functional NAD^+ binding domain comprising the sequence motif
   $PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)
   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

   and

   b) lacks a zinc finger sequence motif of the ~~general~~ formula
   $CX_2CX_mHX_2C$ (SEQ ID NO:30)
   in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.

2. (currently amended) The PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises ~~one of~~ the following ~~general~~ sequence motif~~s~~:
   $(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12) ~~or~~
   ~~$LLWHG(S/T)X_2IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$ (SEQ ID NO:13)~~
   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3. (currently amended) The PARP homolog as claimed in claim 1, further comprising ~~at least another one of~~ the ~~following~~ part-sequence motif~~s~~:
   $LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)~~,~~
   ~~$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),~~

~~QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L (SEQ ID NO:17),~~

~~FYTXIPHXFGX_3PP (SEQ ID NO:18); and~~

~~KX_3LX_2LXDIEXAX_2L (SEQ ID NO:19),~~

in which the X radicals are, independently of one another, any amino acid.

4-32. (canceled)

33. (new) The PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises the following sequence motif:

LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

AX_3FXKX_4KTXNXWX_5FX_3PXK (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

XL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

FYTXIPHXFGX_3PP (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

KX_3LX_2LXDIEXAX_2L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

38. (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a) has a functional NAD^+ binding domain comprising the sequence motif
$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b) lacks a zinc finger sequence motif of the formula
$CX_2CX_mHX_2C$ (SEQ ID NO:30)
in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence motif:
$(L/V)X_6LX_6LX_6L$

wherein X radicals are, independently of one another, any amino acid.

39. (new) The PARP homolog as claimed in claim 38 further comprising at least one of the following part-sequence motifs:

~~$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),~~
$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),
$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),
FYTXIPHXFGX$_3$PP (SEQ ID NO:18), and
$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

40. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$

is closest to the N terminus.

42. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

43. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$

is closest to the N terminus.

44. (new) The PARP homolog as claimed in claim 1 further comprising at least one of the following:

$GX_3LXVALG$,

$GX2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YXYX_3QXYLL$

in which a is 7 to 9 and

X is any amino acid.

45. (new) The PARP homolog as claimed in claim 1 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

46. (new) The PARP homolog as claimed in claim 1 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.

47. (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a) has a functional NAD^+ binding domain comprising the sequence motif

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b) lacks a zinc finger sequence.

48. (new) The PARP homolog as claimed in claim 47 wherein said PARP lacks a zinc finger sequence motif of the formula

$CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49. (new) The PARP homolog as claimed in claim 47 wherein the functional NAD^+ binding domain comprises the following sequence motif:

$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (new) The PARP homolog as claimed in claim 47 wherein the functional NAD^+ binding domain comprises the following sequence motif:

LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

51. (new) The PARP homolog as claimed in claim 47 further comprising a leucine zipper-like sequence:

(L/V)X_6LX_6LX_6L

wherein X radicals are, independently of one another, any amino acid.

52. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following part-sequence motifs:

LX_9NX_2YX_2QLLX(D/E)$X_{10/11}$WGRVG (SEQ ID NO: 15),

AX_3FXKX_4KTXNXWX_5FX_3PXK (SEQ ID NO:16),

QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L (SEQ ID NO:17),

FYTXIPHXFGX_3PP (SEQ ID NO:18), and

KX_3LX_2LXDIEXAX_2L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

53. (new) The PARP homolog as claimed in claim 51 further comprising:

LX_9NX_2YX_2QLLX(D/E)$X_{10/11}$WGRVG (SEQ ID NO: 15),

AX_3FXKX_4KTXNXWX_5FX_3PXK (SEQ ID NO:16),

QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L (SEQ ID NO:17),

FYTXIPHXFGX$_3$PP (SEQ ID NO:18), and

KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

54. (new) The PARP homolog as claimed in claim 51 further comprising:

LX$_9$NX$_2$YX$_2$QLLX(D/E)X$_{10/11}$WGRVG (SEQ ID NO: 15),

AX$_3$FXKX$_4$KTXNXWX$_5$FX$_3$PXK (SEQ ID NO:16),

QXL(I/L)X$_2$IX$_9$MX$_{10}$PLGKLX$_3$QIX$_6$L (SEQ ID NO:17),

FYTXIPHXFGX$_3$PP (SEQ ID NO:18), and

KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX$_9$NX$_2$YX$_2$QLLX(D/E)X$_{10/11}$WGRVG

is closest to the N terminus.

55. (new) The PARP homolog as claimed in claim 47 further comprising at least one of the following:

GX$_3$LXVALG,

GX2SX$_4$GX$_3$PX$_a$LXGX$_2$V, and

E(Y/F)X$_2$YX$_3$QX$_4$YLL

in which a is 7 to 9 and

X is any amino acid.

56. (new) The PARP homolog as claimed in claim 47 further comprising

GX$_3$LXEVALG,

GX$_2$SX$_4$GX$_3$PX$_a$LXGX$_2$V, and

E(Y/F)X$_2$YX$_3$QX$_4$YLL

in which a is 7 to 9 and

X is any amino acid.

57. (new) The PARP homolog as claimed in claim 47 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.

58. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following:

$GX_3LXVALG$,

GX2S$X_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

59. (new) The PARP homolog as claimed in claim 51 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

60. (new) The PARP homolog as claimed in claim 51 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.